

09991157 Results

SEQ ID NO: 119

SUMMARIES

Result No.	% Query					Description
	Score	Match	Length	DB	ID	
1	3402	100.0	3402	6	AR252460	AR252460 Sequence
2	3402	100.0	3402	6	AX080803	AX080803 Sequence
3	3402	100.0	3402	6	AX191426	AX191426 Sequence
4	3402	100.0	3402	6	AX403231	AX403231 Sequence
5	3402	100.0	3402	9	AY358303	AY358303 Homo sapi
6	3350	98.5	3397	6	AX780431	AX780431 Sequence
7	3350	98.5	3397	9	AF312678	AF312678 Homo sapi
8	2817.6	82.8	3305	9	BC036769	BC036769 Homo sapi
9	2816.8	82.8	3080	6	AX287610	AX287610 Sequence
10	2816.8	82.8	3080	9	HSA277437	AJ277437 Homo sapi
11	2815.2	82.8	3112	6	AX287608	AX287608 Sequence
12	2372	69.7	2667	9	BC013955	BC013955 Homo sapi
13	2017.4	59.3	2178	6	AX224732	AX224732 Sequence
14	1898.4	55.8	177950	9	AC019103	AC019103 Homo sapi
15	1733	50.9	1999	6	AX879425	AX879425 Sequence

RESULT 7

AF312678

LOCUS AF312678 3397 bp mRNA linear PRI 02-MAR-2001

DEFINITION Homo sapiens FGF homologous factor receptor (FHFR) mRNA, complete cds.

ACCESSION AF312678

VERSION AF312678.1 GI:13183617

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3397)

AUTHORS Aggarwal, S., Xie, M.-H., Foster, J., Frantz, G., Stinson, J., Corpuz, R.T., Simmons, L., Hillan, K., Yansura, D.G., Vandlen, R.L., Goddard, A.D. and Gurney, A.L.

TITLE FHFR, a novel fibroblast growth factor receptor that uniquely binds the fibroblast growth factor homologous factors

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 3397)

AUTHORS Aggarwal, S., Xie, M.-H., Foster, J., Frantz, G., Stinson, J., Corpuz, R.T., Simmons, L., Hillan, K., Yansura, D.G., Vandlen, R.L., Goddard, A.D. and Gurney, A.L.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-2000) Molecular Biology, Genentech, 1 DNA Way, San Francisco, CA 94080, USA

FEATURES Location/Qualifiers

source

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/organism="Homo sapiens"

/mol_type="mRNA"

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CDS

150..1643

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Qy 1501 GGTCTCCGGCAGCCCCCAGCACTTACTGGGCCAGGCCAGTTGTGTGGCCCTAAGTTGT 1560
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Qy 1741 ACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGACCCCAGGCAGTCTGTGTGTG 1800
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Qy	2101	CGGACACACACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACAC	2160
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Db	2260	GGCGCAGATATGCTGCCTGGACACACGCAGATATGCTGTCTAGTCACACACACGCAGA	2319
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Db	2620	TGCCTCAACACTCACACACGTGCAGATATTGCTGGACACACACATGTGCACAGATATGC	2679
Qy	2701	TGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGC	2760
Db	2680	TGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGC	2739
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Qy	2821	GCCTGGACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGAAGCCTGCAGTACG	2880
Db	2800	GCCTGGACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGAAGCCTGCAGTACG	2859
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Db	2860	TGTGCCGTGAGGCTCATAGTTGATGAGGGACTTTCCCTGCTCCACCGTCACTCCCCAAC	2919
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Db	2920	TCTGCCCGCCTCTGTCCCCGCCTCAGTCCCCGCCTCCATCCCCGCCTCTGTCCCCTGCC	2979
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RESULT 10

HSA277437

LOCUS HSA277437 3080 bp mRNA linear PRI 20-OCT-2000

DEFINITION Homo sapiens mRNA for fibroblast growth factor receptor-like protein 1, (FGFRL1 gene).

ACCESSION AJ277437

VERSION AJ277437.1 GI:10944886

KEYWORDS FGFRL1 gene; fibroblast growth factor receptor-like protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1

AUTHORS Wiedemann, M. and Trueb, B.

TITLE Characterization of a novel protein (FGFRL1) from human cartilage

related to FGF receptors

JOURNAL Genomics 69 (2), 275-279 (2000)

MEDLINE 20487555

PUBMED 11031111

REFERENCE 2 (bases 1 to 3080)

AUTHORS Trueb, B.

TITLE Direct Submission

JOURNAL Submitted (14-APR-2000) Trueb B., M.E. Muller-Institute, University of Bern, P.O. Box 30, CH-3010 Bern, SWITZERLAND

FEATURES

source

Location/Qualifiers

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CDS

23. .1537

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ORIGIN

Query Match      82.8%; Score 2816.8; DB 9; Length 3080;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 7; Indels 209; Gaps 3;

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Qy	969	GTGAAGCCGGTGATCCAGTGGCTGAAGCGCGTGGAGTACGGCGCCGAGGGCCGCCACAAC	1028
Db	842	GTGAAGCCGGTGATCCAGTGGCTGAAGCGCGTGGAGTACGGCGCCGAGGGCCGCCACAAC	901
Qy	1029	TCCACCATCGATGTGGGCGGCCAGAAGTTTGTGGTGCTGCCACGGGTGACGTGTGGTCTG	1088
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Qy	1089	CGGCCCCGACGGCTCCTACCTCAATAAGCTGCTCATCACCCTGCCCCGCCAGGACGATGCG	1148
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Qy	1149	GGCATGTACATCTGCCTTGGCGCCAACACCATGGGCTACAGCTTCCGCAGCGCCTTCCTC	1208
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Qy	1209	ACCGTGCTGCCAGACCCAAAACCGCCAGGGCCACCTGTGGCCTCCTCGTCCTCGGCCACT	1268
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Qy	1329	CTGCTCCTGTGGCTTTGCCAGGCCCAGAAGAAGCCGTGCACCCCCGCGCCTGCCCCCTCC	1388
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Qy	1389	CTGCCTGGGCACCGCCCGCGGGGACGGCCCGCGACCGCAGCGGAGACAAGGACCTTCCC	1448
Db	1262	CTGCCTGGGCACCGCCCGCGGGGACGGCCCGCGACCGCAGCGGAGACAAGGACCTTCCC	1321
Qy	1449	TCGTTGGCCCGCCTCAGCGCTGGCCCTGGTGTGGGGCTGTGTGAGGAGCATGGGTCTCCG	1508
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Qy	1509	GCAGCCCCCAGCACTTACTGGGCCCAGGCCAGTTGCTGGCCCTAAGTTGTACCCCAA	1568
Db	1382	GCAGCCCCCAGCACTTACTGGGCCCAGGCCAGTTGCTGGCCCTAAGTTGTACCCCAA	1441
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Db	1682	CCCCTGGACACACACACAGACACACACTACCTGGATGCATGTATGCACACACATGC	1741
Qy	1869	GCGCACACGTGCTCCCTGAAGGCACACGTACG--CACACGCACATGCACAGATATGCCGC	1926
Db	1742	GCGCACACGTGCTCCCTGAAGGCACACGTACGCAACACGCACATGCACAGATATGCCGC	1801
Qy	1927	CTGGGCGACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGACATGCCAGAACATA	1986
Db	1802	CTGGGCGACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGACATGCCAGAACATA	1861

Qy	1987	CAAGGACATGCTGCCTGAACATACACACGCACACCCATGCGCAGATGTGCTGCCTGGACA	2046
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Qy	2047	CACACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACA	2106
Db	1922	CACACACACACACGGATATGCTGTCTGGACGCACACACGTGCAGATATGGTATCCGGACA	1981
Qy	2107	CACACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACATGC	2166
Db	1982	CACACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACATGC	2041
Qy	2167	ACGGATATTGCCTGGACACACACACACACACGCGTGCACAGATATGCTGTCTGGACAC	2226
Db	2042	ACGGATATTGCCTGG--ACACACACACACACGCGTGCACAGATATGCTGTCTGGACAG	2099
Qy	2227	GCACACACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCGCA	2286
Db	2100	GCACACACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCGCA	2159
Qy	2287	GATATGCTGCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCT	2346
Db	2160	GATATGCTGCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCT	2219
Qy	2347	GTCCGGACACACACACGCATGCACAGATATGCTGTCCGGACACACACGCACGCAGATA	2406
Db	2220	GTCCGGACACACACACGCATGCACAGATATGCTGTCCGGACACACACGCAC-----	2272
Qy	2407	TGCTGCCTGGACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTG	2466
Db	2273	-----	2272
Qy	2467	CCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGC	2526
Db	2273	-----	2272
Qy	2527	TGTCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGAC	2586
Db	2273	-----	2272
Qy	2587	ACACATGCACACACAGGTGCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTC	2646
Db	2273	-----GCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTC	2314
Qy	2647	AACACTCACACACGTGCAGATATTGCCTGGACACACATGTGCACAGATATGCTGTCTG	2706
Db	2315	AACACTCACACACGTGCAGATATTGCCTGGACACACATGTGCACAGATATGCTGTCTG	2374
Qy	2707	GACATGCACACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGCAGATAT	2766
Db	2375	GACATGCACACACGTGCAGATATGCTGTCCGGATACACACGCACGCACACATGCAGATAT	2434
Qy	2767	GCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGTGCAGATATGCTGCCTGG	2826
Db	2435	GCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGTGCAGATATGCTGCCTGG	2494
Qy	2827	ACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCC	2886
Db	2495	ACACACGCAGACTGACGTGCTTTTGGGAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCC	2554
Qy	2887	GTGAGGCTCATAGTTGATGAGGGACTTCCCTGCTCCACCGTCACTCCCCAACTCTGCC	2946
Db	2555	GTGAGGCTCATAGTTGATGAGGGACTTCCCTGCTCCACCGTCACTCCCCAACTCTGCC	2614
Qy	2947	CGCCTCTGTCCCCGCCTCAGTCCCCGCCTCCATCCCCGCCTCTGTCCCCTGGCCTTGGCG	3006
Db	2615	CGCCTCTGTCCCCGCCTCAGTCCCCGCCTCCATCCCCGCCTCTGTCCCCTGGCCTTGGCG	2674
Qy	3007	GCTATTTTTGCCACCTGCCTTGGGTGCCAGGAGTCCCCTACTGCTGTGGGCTGGGGTTG	3066

Db 2675 GCTATTTTGGCCACCTGCCTTGGGTGCCAGGAGTCCCCTACTGCTGTGGGCTGGGGTTG 2734

Qy 3067 GGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAGCCCATGGCTAGTGGCTCATCCCCAGT 3126
 |||||

Db 2735 GGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAGCCCATGGCTAGTGGCTCATCCCCACT 2794

Qy 3127 GCATTCTCCCCCTGACACAGAGAAGGGGCCTTGGTATTTATATTTAAGAAATGAAGATAA 3186
 |||||

Db 2795 GCATTCTCCCCCTGACACAGAGAAGGGGCCTTGGTATTTATATTTAAGAAATGAAGATAA 2854

Qy 3187 TATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGACTGTGGTCTCTCCTGGGGCCCCG 3246
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Db 2855 TATTAATAATGATGGAAGGAAGACTGGGTTGCAGGGACTGTGGTCTCTCCTGGGGCCCCG 2914

Qy 3247 GACCCGCCTGGTCTTTTCAGCCATGCTGATGACCACACCCCGTCCAGGCCAGACACCACCC 3306
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Db 2915 GACCCGCCTGGTCTTTTCAGCCATGCTGATGACCACACCCCGTCCAGGCCAGACACCACCC 2974

Qy 3307 CCCACCCCACTGTCGTGGTGGCCCCAGATCTCTGTAATTTTATGTAGAGTTTGAGCTGAA 3366
 |||||

Db 2975 CCCACCCCACTGTCGTGGTGGCCCCAGATCTCTGTAATTTTATGTAGAGTTTGAGCTGAA 3034

Qy 3367 GCCCCGTATATTTAATTTATTTTGTAAACACAAAA 3402
 |||||

Db 3035 GCCCCGTATATTTAATTTATTTTGTAAACATGAAA 3070

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3402	100.0	3402	3	AAZ64984	Aaz64984 Membrane-
2	3402	100.0	3402	3	AAC58376	Aac58376 Human PRO
3	3402	100.0	3402	5	AAF44130	Aaf44130 Human PRO
4	3402	100.0	3402	6	ABK11750	Abk11750 cDNA enco
5	3402	100.0	3402	6	ABK28591	Abk28591 Human DNA
6	3402	100.0	3402	7	ABX77786	Abx77786 Human PRO
7	3402	100.0	3402	7	ABX80198	Abx80198 Human sec
8	3402	100.0	3402	7	ACA69104	Aca69104 Human cDN
9	3402	100.0	3402	7	ABX90175	Abx90175 Human sec
10	3402	100.0	3402	7	ABX64021	Abx64021 cDNA enco
11	3402	100.0	3402	7	ACA64243	Aca64243 Novel hum
12	3402	100.0	3402	7	ABX80702	Abx80702 Human sec
13	3402	100.0	3402	7	ACD44211	Acd44211 cDNA enco
14	3402	100.0	3402	7	ABX79382	Abx79382 Human sec
15	3402	100.0	3402	7	ACA93403	Aca93403 Novel hum
16	3402	100.0	3402	7	ABX81085	Abx81085 Human sec
17	3402	100.0	3402	7	ACA92901	Aca92901 Novel hum
18	3402	100.0	3402	7	ABX16985	Abx16985 Human PRO
19	3402	100.0	3402	8	ACA67840	Aca67840 Novel hum
20	3402	100.0	3402	8	ACA88289	Aca88289 Human sec
21	3402	100.0	3402	8	ACD81796	Acd81796 cDNA enco
22	3402	100.0	3402	8	ADA37629	Ada37629 Human cDN
23	3402	100.0	3402	8	ADA21315	Ada21315 Human cDN
24	3402	100.0	3402	8	ADA10102	Ada10102 Human cDN
25	3402	100.0	3402	8	ADA17646	Ada17646 cDNA enco
26	3402	100.0	3402	8	ADA27754	Ada27754 Human cDN
27	3402	100.0	3402	8	ADA94334	Ada94334 Human cDN
28	3402	100.0	3402	8	ADA38559	Ada38559 Human cDN
29	3402	100.0	3402	8	ADA92680	Ada92680 Human cDN
30	3402	100.0	3402	8	ACH65357	Ach65357 Human cDN
31	3402	100.0	3402	8	ADA22241	Ada22241 Human cDN
32	3402	100.0	3402	8	ACD39347	Acd39347 Human PRO
33	3402	100.0	3402	8	ADA06407	Ada06407 Human sec
34	3402	100.0	3402	8	ADA39100	Ada39100 Human cDN
35	3402	100.0	3402	8	ADB96126	Adb96126 Human PRO
36	3402	100.0	3402	9	ADC57598	Adc57598 Human PRO
37	3402	100.0	3402	9	ADC54962	Adc54962 Human PRO

38	3402	100.0	3402	9	ADC11829	Adc11829 Human cDN
39	3402	100.0	3402	9	ADC56251	Adc56251 Human PRO
40	3402	100.0	3402	9	ADC07306	Adc07306 Human cDN
41	3402	100.0	3402	9	ADC11296	Adc11296 Human cDN
42	3402	100.0	3402	9	ADC14418	Adc14418 Novel hum
43	3402	100.0	3402	9	ADD07950	Add07950 Novel hum
44	3402	100.0	3402	9	ADC81775	Adc81775 Human PRO
45	3402	100.0	3402	9	ADD07417	Add07417 Novel hum

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1061.2	31.2	1967	3	US-09-383-586-22	Sequence 22, Appl
2	965.8	28.4	1004	3	US-09-383-586-24	Sequence 24, Appl
3	796	23.4	1742	3	US-09-383-586-23	Sequence 23, Appl
4	312.6	9.2	384	3	US-09-383-586-21	Sequence 21, Appl
5	121	3.6	2049	4	US-09-099-749-10	Sequence 10, Appl
6	118.2	3.5	5993	3	US-09-383-630-1	Sequence 1, Appli
7	118.2	3.5	5993	3	US-09-383-630-2	Sequence 2, Appli
8	116.8	3.4	1869	4	US-09-499-846-1	Sequence 1, Appli
9	110.8	3.3	2469	1	US-07-997-133-2	Sequence 2, Appli
10	110.8	3.3	2469	1	US-08-459-296-1	Sequence 1, Appli
11	110.8	3.3	2469	5	US-07-997-133-2	Sequence 2, Appli

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2232	65.6	2530	11	BC015228	BC015228 Homo sapi
2	919.2	27.0	999	12	BM561628	BM561628 AGENCOURT
3	842.6	24.8	907	13	BQ685083	BQ685083 AGENCOURT
4	839.2	24.7	925	13	BQ924530	BQ924530 AGENCOURT
5	824.6	24.2	989	12	BM806988	BM806988 AGENCOURT
6	815.8	24.0	886	13	BU528897	BU528897 AGENCOURT
7	813.6	23.9	906	13	BQ900887	BQ900887 AGENCOURT
8	801	23.5	854	9	AU124593	AU124593 AU124593
9	793.6	23.3	959	13	BQ952255	BQ952255 AGENCOURT

SEQ ID NO: 118

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	520.5	19.2	822	2	B49151	fibroblast growth
2	514.5	19.0	822	2	S19947	fibroblast growth
3	500.5	18.5	812	1	A36477	fibroblast growth
4	500.5	18.5	814	1	A39752	fibroblast growth
5	496.5	18.3	800	2	A48991	heparin-binding gr
6	496.5	18.3	801	2	I55363	fibroblast growth
7	494.5	18.3	800	1	TVHU2F	fibroblast growth
8	488.5	18.0	797	2	S38579	fibroblast growth
9	482	17.8	806	1	TVHUF3	fibroblast growth
10	473	17.5	802	1	TVHUF4	fibroblast growth
11	465.5	17.2	821	1	TVMSBK	fibroblast growth
12	464.5	17.1	480	2	B56182	fibroblast growth
13	464	17.1	806	2	A35963	protein-tyrosine k
14	462	17.1	823	2	B35963	protein-tyrosine k
15	461.5	17.0	821	1	TVHUF2	fibroblast growth
16	457	16.9	829	2	JC4583	fibroblast growth
17	455.5	16.8	818	2	JC4058	fibroblast growth

RESULT 1

B49151

fibroblast growth factor receptor 4 - Iberian ribbed newt

C;Species: Pleurodeles waltl (Iberian ribbed newt)

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C;Accession: B49151

R;Shi, D.L.; Feige, J.J.; Riou, J.F.; DeSimone, D.W.; Boucaut, J.C.

Development 116, 261-273, 1992

A;Title: Differential expression and regulation of two distinct fibroblast growth factor receptors during early development of the urodele amphibian Pleurodeles waltl.

A;Reference number: A49151; MUID:93130775; PMID:1483392

A;Accession: B49151

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-822 <SHI>

A;Cross-references: GB:X65059; NID:g64252; PIDN:CAA46192.1; PID:g64253

A;Experimental source: tail-bud

A;Note: sequence extracted from NCBI backbone (NCBIN:122598, NCBIP:122599)

C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein kinase homology

C;Keywords: ATP; growth factor receptor

F;283-354/Domain: immunoglobulin homology <IMM>

F;484-769/Domain: protein kinase homology <KIN>

F;492-500/Region: protein kinase ATP-binding motif

Query Match 19.2%; Score 520.5; DB 2; Length 822;

Best Local Similarity 30.7%; Pred. No. 5.5e-25;

Matches 139; Conservative 83; Mismatches 166; Indels 65; Gaps 17;

```
Qy      2 TPSPLLLLLLPPLLGAFPAAAAARGPPK----MADKVVPQVARL--GRTVRLQCPV 53
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      15 TTRPLALLLCGLL--AFSALSCARTLPEGRKANLAELVSEEEHFLDPGNALRLFC-- 69

Qy      54 EGDPPPLTMW-TKDGRTIHSGWSRFRVLPQGLKVQVEREDAGVYVCKATNGFGSLSVNY 112
      : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db      70 DTNQTTIVNWYTESTRLQHGG--RIRLTDTVLEIADVITYEDSGLYLC-VVPGTGHLRNF 126

Qy     113 TLVVLDLDDISPG--KESLGPDSSSG--GQEDPASQQWARPRFTQPSKMRRRVIARPVGSS 167
      | : | | : | | | | | | | | | | | | | | | | | | | | |
Db     127 TISVVDLSLAGDDDDHDHGREDSDAGMDGPPYSTSYRAPFWSQPQRMDDKKLYAVPAGNT 186

Qy     168 VRLKCVASGHPRPDITWMKDDQAL---TRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVS 224
      | : | | : | | | | | | | | | | | | | | | | | | | | |
Db     187 VKFRCPASAGNPTPGIRWLKNGREFGGEHRIGGIRLRHQHWSLVMSVVPSPDRGNYTCLVE 246
```

Qy	225	NRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRV	284
		: : : : : : : : : : : : : : :	
Db	247	NKFGSISYSYLDDVLEERSPHRPILQAGLPANTTTAMLGSDVQFFCKVYSDAQPHIQWLKHI	306
Qy	285	E-----YGAEGRHNSTIDVGQGKFV-VLPTGDVWSRPGDSYLNKLITRARQDDAGMYIC	338
		: : : : : : :	
Db	307	EVNGSRYPGD-----GVPFVQVLKTADI---NSSEVEVLYLHNVSFEDAGEYTTC	352
Qy	339	LGANTMGYSFRSAFLTIVLPD----PKPPGPPVASSSSATSLPWFPVIGIPAGAVFILGTL	394
		: : : : : : : : : : : : : :	
Db	353	LGN SIGLSYQS A WL TV L P E E D F A K E A E G P E T R Y T D -----I I I Y T S G S L A L L M A A V	404
Qy	395	LLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRS	427
		: : :	
Db	405	IVVLCRMQ-----LPPTKTHLEPATVHKLS	429

Qy 395 LLWLCQAQKKPCTPAPAPPLPGHRPPGTARDS 427
 :: ||: | || | | |
 Db 405 IVVLCRMQ-----LPPTKTHLEPATVHKLS 429

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						
1	500.5	18.5	812	1	FGR1_XENLA	P22182 xenopus lae
2	496.5	18.3	801	1	FGR3_MOUSE	Q61851 mus musculu
3	482	17.8	806	1	FGR3_HUMAN	P22607 homo sapien
4	473	17.5	802	1	FGR4_HUMAN	P22455 homo sapien
5	464	17.1	806	1	CEK2_CHICK	P18460 gallus gall
6	462	17.1	823	1	CEK3_CHICK	P18461 gallus gall
7	461.5	17.0	821	1	FGR2_HUMAN	P21802 homo sapien
8	460.5	17.0	821	1	FGR2_MOUSE	P21803 mus musculu
9	455.5	16.8	819	1	FGR1_CHICK	P21804 gallus gall
10	445.5	16.4	808	1	FGR4_MOUSE	Q03142 mus musculu
11	436	16.1	813	1	FGR2_XENLA	Q03364 xenopus lae

RESULT 1

FGR1_XENLA

ID FGR1_XENLA STANDARD; PRT; 812 AA.
 AC P22182;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibroblast growth factor receptor 1 precursor (EC 2.7.1.112).
 GN FGFR-1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045998; PubMed=2172985;
 RA Musci T.J., Amaya E., Kirschner M.W.;
 RT "Regulation of the fibroblast growth factor receptor in early Xenopus
 RT embryos."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8365-8369(1990).
 CC -!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
 CC family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U24491; AAA86868.1; -.
 DR PIR; A36477; A36477.
 DR HSSP; P11362; 1FGK.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGc2; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Repeat; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 812 FIBROBLAST GROWTH FACTOR RECEPTOR 1.
FT DOMAIN 21 371 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 372 393 POTENTIAL.
FT DOMAIN 394 812 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 110 IG-LIKE C2-TYPE 1.
FT DOMAIN 154 242 IG-LIKE C2-TYPE 2.
FT DOMAIN 251 353 IG-LIKE C2-TYPE 3.
FT DOMAIN 472 761 PROTEIN KINASE.
FT NP_BIND 478 486 ATP (BY SIMILARITY).
FT BINDING 508 508 ATP (BY SIMILARITY).
FT ACT_SITE 617 617 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 812 AA; 90502 MW; B06333BAFEAC5C9B CRC64;

Query Match 18.5%; Score 500.5; DB 1; Length 812;
Best Local Similarity 30.5%; Pred. No. 1e-23;
Matches 145; Conservative 78; Mismatches 192; Indels 61; Gaps 17;

Qy 9 LLLPPLLGAFFPAAAAARGPPKMAKVPR-----QVARLGRTVRLQCPVEGDPPLT 61
| | | : | | | : | | : | : | : | : | : | : | :
Db 7 LLLGWVLLGA--ALSVARPPSTLPDEVAPKTKTEVEFYSAQPGDRITLQCRLEDVQSIN 64
Qy 62 MWTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTL---VVLD 118
| | : | : | : | : | : | : | : | : | : | : | : | :
Db 65 -WVKNQVQL-SETNRTRITGEEI QISNAGPEDNGVYAC-VTNG---PSRTYTVLCSVNVS 118
Qy 119 DISPGKESLGPDSSSGQEDPASQQWA--RPRFTQPSKMRRRVIAIPVGVSSVRLKCVASG 176
| | | | : | : | : | : | : | : | : | : | : | : | :
Db 119 DALPSAEDDDDDDDNSSEEKAAENSKPNRPLWSHPEKMEKKLHAVPAAKTVKFRCPANG 178
Qy 177 HRPDPITWMKDDQALTRPE---AAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINAT 233
| | : | : | : | : | : | : | : | : | : | : | : | :
Db 179 TPTPTLRWLKNNRAQQDQRIGGYKVRSTQWLSLIMDSVVPDCKGNYTCIVENKYGAINHT 238
Qy 234 YKVDVIQRTSRKPVLTGTHPVNTTDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRH 293
| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 239 YQLDVVERSPHRPILQAGLPANTSVTVGTAEFSCKVYSDPQPHIQWLRHIEI-----NG 293
Qy 294 STIDVGQKQFV-VLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAF 352
| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 294 SRVASDGFPPYVEILKTAGV--NTSDKMEVLHLNRNVTFEDAGQYTCLAANSIGISHSAW 351
Qy 353 LTVL--PDPKPPGPPVASSSSATSLPWVVGIPAGAVFILGTLTLLWLCAQKKPCTPAP 410
| | | | | : | : | : | : | : | : | : | : | : | :
Db 352 LTVLKVEDNKP-----ALLASPLQLEIII-YCTGAAFVSAMVVTIIIFKMKHPSKKSD 403
Qy 411 -----APPLPGHRPPGTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAP 456
| : | : | : | : | : | : | : | : | : | : | : | : | :
Db 404 FNSQLAVHKLAKSIPVRRQVTVSGDSSS-----SMNSGVILVRRLLSSSGTP 449

RESULT 2

FGR3_MOUSE

ID FGR3_MOUSE STANDARD; PRT; 801 AA.
AC Q61851; Q61564; Q63834;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibroblast growth factor receptor 3 precursor (EC 2.7.1.112) (FGFR-3)
DE (Heparin-binding growth factor receptor).
GN FGFR3 OR MFR3 OR SAM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92355591; PubMed=1379594;
RA Ornitz D.M., Leder P.;
RT "Ligand specificity and heparin dependence of fibroblast growth
RT factor receptors 1 and 3.";
RL J. Biol. Chem. 267:16305-16311(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=93177694; PubMed=8382556;
RA Katoh O., Hattori Y., Sasaki H., Sakamoto H., Fujimoto K.,
RA Fujii T., Sugimura T., Terada M.;
RT "Isolation of the complementary DNA encoding a mouse heparin-binding
RT growth factor receptor with the use of a unique kinase insert
RT sequence.";
RL Cancer Res. 53:1136-1141(1993).
RN [3]
RP SEQUENCE OF 242-364 FROM N.A. (ISOFORM 2).
RX MEDLINE=94209351; PubMed=7512569;
RA Chellaiah A.T., McEwen D.G., Werner S., Xu J., Ornitz D.M.;
RT "Fibroblast growth factor receptor (FGFR) 3. Alternative splicing in
RT immunoglobulin-like domain III creates a receptor highly specific for
RT acidic FGF/FGF-1.";
RL J. Biol. Chem. 269:11620-11627(1994).
CC -!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.
CC PREFERENTIALLY BINDS FGF1.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=IIIc;
CC IsoId=Q61851-1; Sequence=Displayed;
CC Name=2; Synonyms=IIIB;
CC IsoId=Q61851-2; Sequence=VSP_002990;
CC -!- TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN HEART, LUNG, KIDNEY,
CC SKIN, HEAD AND LIVER BUT NOT IN MUSCLE. IN ADULT, HIGHEST LEVELS
CC IN BRAIN. ALSO EXPRESSED IN LIVER, LUNG, KIDNEY, TESTIS, OVARY AND
CC UTERUS. VERY LOW LEVELS IN HEART, THYMUS, SPLEEN AND MUSCLE.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO FROM MID-GESTATION AND IN
CC ADULT.
CC -!- SIMILARITY: Belongs to the fibroblast growth factor receptor
CC family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M81342; AAA39535.1; -.

Qy 185 MKDDQALT---RPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQR 241
 Db 183 LKNGKEFRGEHRIGGIKLRHQQWSLVMSVPSDRGNYTCVVENKFGSIRQTYTLDVLER 242
 Qy 242 TRSKPVLGTGTHPVNTTVDFGGTTSFQCKVRSVDKVPVIQWLKRVEYGAEGRHNSTIDVGGQ 301
 Db 243 SPHRPILQAGLPANQTAILGSDVEFHCKVYSDAQPHIQWLKHVEV-----NGSKVGPDPGT 297
 Qy 302 KfV-VLPTGDVWSRPPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVLP-DP 359
 Db 298 PYVTVLKTAG--ANTTDKELEVLSLHNVTTFEDAGEYTCLAGNSIGFSHSAWLVLPAEE 355
 Qy 360 KPPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLLEWLCAQKKPCTPAPAPPL----- 414
 Db 356 ELMETDEAGSVYAGVLSYGVVF-----FLFILVVAIVLCRLRSPPKKGLGSPTVHKVSR 410
 Qy 415 -PGHRPPTARDRSGDKDLP--SLAALSAGPGVGLC--EEHGSAPAPQ 457
 Db 411 FPLKRQVSLESNSSMNSNTPLVRIARLSSGEGPVLANVSELELPADPK 458

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2709	100.0	504	4	Q8N441	Q8n441 homo sapien
2	2701	99.7	504	4	Q9H4D7	Q9h4d7 homo sapien
3	2654.5	98.0	497	4	Q9BXN7	Q9bxn7 homo sapien
4	2314.5	85.4	529	11	Q7TQM3	Q7tqm3 rattus norv
5	2308.5	85.2	529	11	Q91V87	Q91v87 mus musculu
6	2255.5	83.3	509	11	Q920C2	Q920c2 mus musculu
7	1860.5	68.7	487	13	Q7T2H2	Q7t2h2 gallus gall
8	1784	65.9	438	11	Q920C3	Q920c3 mus musculu
9	1692	62.5	483	13	Q7SX76	Q7sx76 brachydanio
10	526.5	19.4	800	13	Q9I8X3	Q9i8x3 brachydanio
11	520.5	19.2	822	13	Q91288	Q91288 pleurodeles
12	500.5	18.5	814	13	Q91897	Q91897 xenopus lae
13	498.5	18.4	810	13	Q9PS96	Q9ps96 xenopus lae
14	496.5	18.3	800	11	Q7TSI8	Q7tsi8 mus musculu
15	494.5	18.3	800	11	Q99052	Q99052 mus musculu
16	488.5	18.0	796	13	Q91287	Q91287 pleurodeles
17	481.5	17.8	802	6	Q95M13	Q95m13 bos taurus
18	479	17.7	800	11	Q9JHX9	Q9jhx9 rattus norv

RESULT 1

Q8N441
 ID Q8N441 PRELIMINARY; PRT; 504 AA.
 AC Q8N441;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC036769; AAH36769.1; -.
 DR Genew; HGNC:3693; FGFR1.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGc2; 3.

DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 504 AA; 54536 MW; 56E35E57D5FC141B CRC64;

Query Match 100.0%; Score 2709; DB 4; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.2e-206;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MTPSPLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPL 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MTPSPLLLLLLPPLLGAFFPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPL 60

Qy     61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDI 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDI 120

Qy    121 SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP 180

Qy    181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240

Qy    241 RTRSKPVLGTGTHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 RTRSKPVLGTGTHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG 300

Qy    301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK 360

Qy    361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLWLWCQAQKKPCTPAPAPPLPGHRPP 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLWLWCQAQKKPCTPAPAPPLPGHRPP 420

Qy    421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHT 480

Qy    481 HTHTHSHTHSHVEGKVVHQHIHYQC 504
         ||||||||||||||||||||
Db    481 HTHTHSHTHSHVEGKVVHQHIHYQC 504
```

RESULT 2

Q9H4D7

ID Q9H4D7 PRELIMINARY; PRT; 504 AA.

AC Q9H4D7;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE FGFR-like protein precursor (Fibroblast growth factor receptor
5).

GN FGFR1 OR FGFR5.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cartilage;

RX PubMed=11031111;

RA Wiedemann M., Trueb B.;

RT "Characterization of a novel protein (FGFR1) from human cartilage
related to FGF receptors.";

RL Genomics 69:275-279(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21167383; PubMed=11267671;

RA Kim I., Moon S.O., Yu K.H., Kim U.H., Koh G.Y.;
 RT "A novel fibroblast growth factor receptor-5 preferentially expressed
 RT in the pancreas.";
 RL Biochim. Biophys. Acta 1518:152-156(2001).
 DR EMBL; AJ277437; CAC14171.1; -.
 DR EMBL; AF279689; AAK26742.1; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005007; F:fibroblast growth factor receptor activity; NAS.
 DR GO; GO:0001558; P:regulation of cell growth; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00408; IGc2; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Immunoglobulin domain; Receptor; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 SQ SEQUENCE 504 AA; 54567 MW; 16382E57D4276485 CRC64;

Query Match 99.7%; Score 2701; DB 4; Length 504;
 Best Local Similarity 99.8%; Pred. No. 9.3e-206;
 Matches 503; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MTPSPLLLLLLPLLLLGAFPPAAAAARGPPKMADKVVP	60
Db	1	MTPSPLLLLLLPLLLLGAFPPAAAAARGPPKMADKVVP	60
Qy	61	TMWTKDGRTIHSWRSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Db	61	TMWTKDGRTIHSWRSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Qy	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Db	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRP	180
Qy	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Db	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Qy	241	RTRSKPVLGTGTHPVNTTVDFTGTTSFQCKVRSVDPKPIQWLKRVEYGAEGRHNSTIDVGG	300
Db	241	RTRSKPVLGTGTHPVNTTVDFTGTTSFQCKVRSVDPKPIQWLKRVEYGAEGRHNSTIDVGG	300
Qy	301	QKFVVLPTGDVWSRDPGGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360
Db	301	QKFVVLPTGDVWSRDPGGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360
Qy	361	PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTLWLCAQKKPCTPAPAPPLPGHRPP	420
Db	361	PQGPPVASSSSATSLPWPVVIGIPAGAVFILGTLWLCAQKKPCTPAPAPPLPGHRPP	420
Qy	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHT	480
Db	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHT	480
Qy	481	HTHTSHSHSHVEGKVVHQHIHYQC	504
Db	481	HTHTSHSHSHVEGKVVHQHIHYQC	504

RESULT 3

Q9BXN7

ID Q9BXN7 PRELIMINARY; PRT; 497 AA.

AC Q9BXN7;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE FGF homologous factor receptor.

GN FHFR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Aggarwal S., Xie M.-H., Foster J., Frantz G., Stinson J., Corpuz R.T.,
 RA Simmons L., Hillan K., Yansura D.G., Vandlen R.L., Goddard A.D.,
 RA Gurney A.L.;
 RT "FHFR, a novel fibroblast growth factor receptor that uniquely binds
 RT the fibroblast growth factor homologous factors.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF312678; AAK15273.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00408; IGc2; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 497 AA; 53757 MW; 57301F4F36357360 CRC64;

Query Match 98.0%; Score 2654.5; DB 4; Length 497;
 Best Local Similarity 98.6%; Pred. No. 4.4e-202;
 Matches 497; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

Qy	1	MTFSPLLLLLLPPLLLGAFPPAAAARGPPKMDKVVPQVARLGRTVRLQCPVEGDPPL	60
Db	1	MTFSPLLLLLLPPLLLGAFPPAAAARGPPKMDKVVPQVARLGRTVRLQCPVEGDPPL	60
Qy	61	TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Db	61	TMWTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDI	120
Qy	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIAIPVGSSVRLKCVASGHPRP	180
Db	121	SPGKESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIAIPVGSSVRLKCVASGHPRP	180
Qy	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Db	181	DITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ	240
Qy	241	RTRSKPVLGTGTHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG	300
Db	241	RTRSKPVLGTGTHPVNTTVDFGGTTSFQCKVRSVDVKPVIQWLKRVEYGAEGRHNSTIDVGG	300
Qy	301	QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360
Db	301	QKFVVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPK	360
Qy	361	PPGPPVASSSSATSLPWPVVIGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGHRPP	420
Db	361	PPGPPVASSSSAT-----IGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGHRPP	413
Qy	421	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	480
Db	414	GTARDRSGDKDLPSLAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHT	473
Qy	481	HTHTSHSHSHVEGKVHQHIHYQC	504
Db	474	HTHTSHSHSHVEGKVHQHIHYQC	497